AMENDMENTS TO THE CLAIMS

1. (Currently amended) A computer-based method for identifying conserved peptide motifs useful as drug targets for use in a host organism, wherein said method comprises the steps of:

i) computationally generating overlapping peptide sequences from selected pathogenic organisms of length 'N',

ii) computationally sorting the peptide sequences of length 'N' according to amino acid sequence,

iii) computationally matching the sorted peptide sequences of length 'N' of the selected pathogenic organisms to produce matched common peptide sequences,

iv) computationally locating the matched common peptide sequences in their corresponding protein sequences to provide locations of said matched common peptide sequences and subsequently labeling the matched common peptide sequences with their origin and location;

v) computationally joining overlapping common peptide sequences to obtain extended conserved peptide sequences; ~~and~~

vi) comparing said extended conserved peptide sequences obtained in step (v) to host organism protein sequences to determine which of said conserved peptide sequences from said selected pathogenic organisms are not present in host proteins~~, wherein said conserved peptide sequences which are not present in host proteins are useful as drug targets~~ ; and

vii) communicating said conserved peptide sequences from said selected pathogenic organisms not present in said host proteins to a user.

2. (Previously presented) The method of claim 1, wherein 'N' is at least 4.

3. (Previously presented) The method of claim 1 wherein the selected pathogenic organisms include at least one of: Mycoplasma pneumoniae, Helicobacter pylori, Hemophilus influenzae, Mycobacterium tuberculosis, Mycoplasma genitalium, Bacillus subtilis, and Escherichia coli.

4. (Currently amended) The method of claim 1, wherein the extended conserved peptide sequences comprise one or more of the following sequences:

1. AAQSIGEPGTQLT (SEQ ID NO:1)
2. AGDGTTTAT (SEQ ID NO:2)
3. AGRHGNKG (SEQ ID NO:3)
4. AHIDAGKTTT (SEQ ID NO:4)
5. CPIETPEG (SEQ ID NO:5)
6. DEPSIGLH (SEQ ID NO:6)
7. DEPTSALD (SEQ ID NO:7)
8. DEPTTALDVT (SEQ ID NO:8)
9. DHAGIATQ (SEQ ID NO:9)
10. DHPHGGGEG (SEQ ID NO:10)
11. DLGGGTFD (SEQ ID NO:11)
12. DVLDTWFSS (SEQ ID NO:12)
13. ERERGITI (SEQ ID NO:13)
14. ERGITITSAAT (SEQ ID NO:14)
15. ESRRIDNQLRGR (SEQ ID NO:15)
16. FSGGQRQR (SEQ ID NO:16)
17. GEPGVGKTA (SEQ ID NO:17)
18. GFDYLRDN (SEQ ID NO:18)
19. GHNLQEHS (SEQ ID NO:19)
20. GIDLGTTNS (SEQ ID NO:20)
21. GINLLREGLD (SEQ ID NO:21)
22. GIVGLPNVGKS (SEQ ID NO:22)
23. GKSSLLNA (SEQ ID NO:23)
24. GLTGRKIIVDTYG (SEQ ID NO:24)
25. GPPGTGKTLLA (SEQ ID NO:25)
26. GPPGVGKT (SEQ ID NO:26)
27. GSGKTTLL (SEQ ID NO:27)
28. GTRIFGPV (SEQ ID NO: 28)
29. IDTPGHVDFT (SEQ ID NO:29)
30. ILAHIDHGKSTL (SEQ ID NO:30)
31. INGFGRIGR (SEQ ID NO:31)
32. IREGGRTVG (SEQ ID NO:32)
33. IVGESGSGKS (SEQ ID NO:33)
35. KMSKSKGN (SEQ ID NO:35)
36. KMSKSLGN (SEQ ID NO:36)
37. KNMITGAAQMDGAIL (SEQ ID NO:37)
38. KPNSALRK (SEQ ID NO:38)
39. LFGGAGVGKTV (SEQ ID NO:39)
40. LGPSGCGK (SEQ ID NO:40)
41. LHAGGKFD (SEQ ID NO:41)
42. LIDEARTPLIISG (SEQ ID NO:42)
43. LLNRAPTLH (SEQ ID NO:43)
44. LPDKAIDLIDE (SEQ ID NO:44)
45. LPGKLADC (SEQ ID NO:45)
46. LSGGQQQR (SEQ ID NO:46)
47. MGHVDHGKT (SEQ ID NO:47)
48. NADFDGDQMAVH (SEQ ID NO:48)
49. NGAGKSTL (SEQ ID NO:49)
50. NLLGKRVD (SEQ ID NO:50)
51. NTDAEGRL (SEQ ID NO:51)
52. PSAVGYQPTLA (SEQ ID NO:52)
53. QRVALARA (SEQ ID NO:53)
54. QRYKGLGEM (SEQ ID NO:54)
55. RDGLKPVHRR (SEQ ID NO:55)
56. SALDVSIQA (SEQ ID NO:56)
57. SGGLHGVG (SEQ ID NO:57)
58. SGSGKSSL (SEQ ID NO:58)
59. SGSGKSTL (SEQ ID NO:59)
60. SVFAGVGERTREGND (SEQ ID NO:60)
61. TGRTHQIRVH (SEQ ID NO:61)
62. TGVSGSGKS (SEQ ID NO:62)
63. TLSGGEAQRI (SEQ ID NO: 63)
64. TNKYAEGYP (SEQ ID NO:64)
65. TPRSNPATY (SEQ ID NO:65)
66. VEGDSAGG (SEQ ID NO:66); and
67. VRKRPGMYIG (SEQ ID NO:67)

34. KFSTYATWWI (SEQ ID NO:34)

5. (Canceled)

6. (Currently amended) The method of any one of claims 1-4 wherein the conserved peptide sequences are found within the sequences of at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN
II EXONUCLEASE ABC SUBUNIT A
III EXONUCLEASE ABC SUBUNIT B
IV DNA GYRASE SUBUNIT B
V ATP SYNTHASE BETA CHAIN
VI S-ADENOSYLMETHIONINE SYNTHETASE
VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
VIII ELONGATION FACTOR G (EF-G)
IX ELONGATION FACTOR TU (EF-TU)
X 30S RIBOSOMAL PROTEIN S12
XI 50S RIBOSOMAL PROTEIN L12
XII 50S RIBOSOMAL PROTEIN L14
XIII VALYL tRNA SYNTHETASE
XIV CELL DIVISION PROTEIN FtSH HOMOLOG
XV DnaK PROTEIN (HSP70)
XVI GTP BINDING PROTEIN LepA; and
XVII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN OPPF.

7. (Currently amended) The method of claim 1, wherein step (iii) comprises: selecting organism names from a menu;

iteratively comparing peptide sequences of a first organism to sorted peptide sequences of a second organism; and[[,]]

~~for matching sequences,~~ writing matched sequences to a first file for the first organism and to a second file for the second organism.

8. (Currently amended) The method of claim 1 wherein step (iv) comprises:

selecting protein sequences;

iteratively ~~comparing~~ locating matched peptide sequences ~~to~~ in the selected protein sequences; and

if the matched peptide is found in [[a]] one of the selected protein ~~sequence~~ sequences, labeling the matched peptide sequence in a file associated with the selected protein sequence with: a) a protein identification number (PID), b) a location in the protein sequence, and c) a name of a pathogenic organism chosen from the group of selected pathogenic organisms of step iii).

9. (Currently amended) The method of claim 1, wherein said overlapping common peptide sequences in step (v) ~~comprises~~ are computationally joined by:

iteratively comparing matched peptide sequences on matched peptide locations;

determining overlapping matched common peptides; and

determining extended conserved peptide sequences based on overlapping matched ~~peptide sequences~~ common peptides.

10-12. (Canceled)